

100-443887-100

QY	121	TLVMEPSLCEBRLNTLRYLLYLHRAKKELGMRADVSNANVLLIGFSCISLCLICIGI
Db	121	TLVMEPSLCEBRLNTLRYLLYLHRAKKELGMRADVSNANVLLIGFSCISLCLICIGI
QY	181	YEHMTPEQAYYYCCFILLTLTIGEDVYALAKDQALQTPQYVAFSEVYLLTGLTLV

```

#USE      STANDARD;      PRF:      409 AA.
035163;
-2001 (Rel. 40, Created)
-2001 (Rel. 40, last sequence update)
-2001 (Rel. 40, last annotation update)
um channel subfamily K member 3 (acid-sensitive potassium
protein TASK) (TWIK-related acid-sensitive K+ channel)
ic two-pore background K+ channel) (TRAK-1).
DR TASK OR CTBAK.
iculus (mouse).
Xta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Xta; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
XID: 000090;

```

HE FROM N.A.
HEART;
98165556; PubMed-9506712;
Fujita A., Horio Y., Kurachi Y.;
ing and functional expression of a novel cardiac two-pore
K+ channel (CTBAK-1).
Res. 82:513-518(1998).

IE FROM N.A.
Heart;
=20287574; PubMed=10748056;
M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.: "The
block and voltage gating are potassium-dependent in the
leak channel K_{CNK3} ".
Chem. 275:16369-16378(2000).

15-97459932, PubMed-9312005.
F., Leearge F., Fink M., Reyes R., Heurteaux C., Lazdunski M.,
A human background K⁺ channel to sense external
physiological pH." *Proc Natl Acad Sci USA* 94:15546-15551 (1997)

CTION: pH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN INWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW. IN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD SIMILARITY).

UNIT: HOMODIMER (POTENTIAL).

CELLULAR LOCATION: Integral membrane protein (potential).

SITE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL INTESTINE AND STOMACH, NOT DETECTED IN LIVER, THYROID OR SPLEEN.

CELLULOSES: INACTIVATED BY BARIUM.

ILIARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.

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DR	EMBL: AB0008537.	BAA25436.1.	-	
DR	EMBL: AF241598.	AAF81418.1.	-	
DR	EMBL: AF242508.	AAF81418.1.	JOINED.	
DR	EMBL: AF065162.	AAG29339.1.	-	
DR	EMBL: AF006824.	AAG35367.1.	-	
DR	EMBL: AB013345.	BAA28349.1.	-	
DR	MGD: MGT:1100509.	KCKK3.		
DR	InterPro: IPR003280.	K+Channel_2pore.		
DR	InterPro: IPR001622.	K+Channel_pore.		
DR	InterPro: IPR000636.	M+channel_nlg.		
DR	InterPro: IPR003092.	TASK Channel.		
DR	Pfam: PF005420.	Ion_trans_1.		
DR	PRINTS: PRO1333.	2PORECHANNEL.		
DR	PRINTS: PRO1095.	TASKCHANNEL.		
DR	Ionc Channel: Transmembrane.	Ion transport: Potassium transport.		
KM	Glycoprotein.			
FT	DOMAIN	1	8	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	9	29	POTENTIAL.
FT	DOMAIN	78	101	PORE-FORMING 1 (POTENTIAL).
FT	TRANSMEM	108	128	POTENTIAL.
FT	DOMAIN	129	158	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	159	179	POTENTIAL.
FT	DOMAIN	184	207	PORE-FORMING 2 (POTENTIAL).
FT	TRANSMEM	223	243	POTENTIAL.
FT	DOMAIN	244	409	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	53	53	N-LINKED (GLCNAc. . .) (POTENTIAL
FT	CONFLICT	4	4	O -> E (IN REF. 3).
FT	CONFLICT	123	123	V -> I (IN REF. 3).
SQ	SEQUENCE	409 AA:	43068 MW:	35236ED01AAC5687 CRC64:

Query Match	90.18;	Score 1840.5;	DB 1;	Length 409;
Best Local Similarity	88.58;	Pred. No. 8.1e-138;		
Matches 362;	Conservative	7;	Mismatches 25;	Indels 15;

QY	1	MRQNRRTALALVCFEFTLLGAAVPALESSEPLETEROLELROOLELARN	
Db	1	MRQNRRTALALVCFEFTLLGAAVPALESSEPLETEROLELROOLELARN	
QY	61	EKEERVYLRKPKKGVQVORFAGSFYFATYITTTIGGHAAPSDGGKVCMMY	
Db	61	EKEERVYLRKPKKGVQVORFAGSFYFATYITTTIGGHAAPSDGGKVCMMY	
QY	121	TVLNFQSGERINELVRYLLHRANKGLGNRADVSHANNVLTGFESCISTLCI	
Db	121	TVLNFQSGERINELVRYLLHRANKGLGNRAEVSANNVLTGFESCISTLCI	
QY	181	YEHMFEPQAYYYCFETLTCTTGIGDGYVALOKDOLQTOPVAFSPYILTGLT	
Db	181	YEHMFEPQAYYYCFETLTCTTGIGDGYVALOKDOLQTOPVAFSPYILTGLT	
QY	241	LVLEFPTWNADEKRDENRALLTRNGQAGGGG-----GGSAMTTDTA	
Db	241	LVLEFPTWNADEKRDENRALLTRNGQAVGGGSLGSGDVRPDDPV	
QY	292	-----GGGGRRNYAEVLNFQSGSCSLTKYSREKLOYSTIPHLIPDLSSTPT	
Db	301	GVCVGVGSSGRNRYAEVLNFQSGSCSLTKYSREKLOYSTIPHLIPDLSSTPT	
QY	346	SPGGGGRRSDTPSRRCICSGAPNSAISVSTGLSLSTRGMLKRRSSV 394	
Db	361	SPGGGGRRSDTPSRRCICSGORSAISVSTGLSLSLAARGMLKRRSSV 409	

date]